

AMENDMENTS TO THE CLAIMS

This claim listing will replace all prior versions, and listings, of the claims in the application.

Listing of the Claims:

1-8. (canceled)

9. (currently amended) A process of producing a huE3 α polypeptide comprising ~~culturing the host cell of claim 5 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture;~~

a.) inserting an isolated nucleic acid molecule encoding a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2 into a vector;

b.) inserting said vector into a host cell;

c.) culturing said host cell under suitable conditions to express the polypeptide; and

d.) optionally isolating the polypeptide from the cultured host cell.

10-11. (canceled)

12. (currently amended) A process for determining whether a compound inhibits huE3 α polypeptide activity or production comprising exposing a host cell according to ~~claims 5, 6, or 7~~ 2 to the compound, and measuring huE3 α polypeptide activity or production in said host cell.

13. (currently amended) An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NOS: ~~2 or 4~~.

14. (currently amended) An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) the mature amino acid sequence as set forth in SEQ ID NOS: ~~2 or 4~~ comprising a mature amino terminus at residue 1, optionally further comprising an amino-terminal methionine;

- (b) an amino acid sequence for an ortholog of SEQ ID NOS: 2 ~~or~~ 4;
- (c) an amino acid sequence that is at least about 70, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the amino acid sequence of SEQ ID NOS: 2 ~~or~~ 4, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4;
- (d) a fragment of the amino acid sequence set forth in SEQ ID NOS: 2 ~~or~~ 4 comprising at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4;
- (e) an amino acid sequence for an allelic variant or splice variant of either the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4, or at least one of (a)-(c).

15. (canceled)

16. (currently amended) An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4;
- (b) the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4 with at least one amino acid insertion, wherein the polypeptide has an activity of a polypeptide comprising the amino acid sequence set forth in SEQ ID NOS: 2 ~~or~~ 4;
- (c) the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4;
- (d) the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4 which has a C- and/or N- terminal truncation, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4; and
- (e) the amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4, with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NOS: 2 ~~or~~ 4.

17. (currently amended) An isolated polypeptide encoded by the nucleic acid molecule of ~~claims 1, 2, or 3~~ comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence as set forth in SEQ ID NO: 1;

(b) a nucleotide sequence encoding the polypeptide set forth in SEQ ID NOS: 2;

(c) a nucleotide sequence which hybridizes under highly stringent conditions to the complement of (a) or (b); and

(d) a nucleotide sequence complementary to any of (a)-(c).

18. (original) The isolated polypeptide according to claim 14 wherein the percent identity is determined using a computer program selected from the group consisting of GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith-Waterman algorithm.

19-39. (canceled)

40. (original) A composition comprising the polypeptide of claims 13, 14, or 16 and a pharmaceutically acceptable formulation agent.

41. (original) The composition of claim 40 wherein the pharmaceutically acceptable formulation agent is a carrier, adjuvant, solubilizer, stabilizer, or anti-oxidant.

42. (currently amended) The composition of claim 40 wherein the polypeptide comprises the mature amino acid sequence as set forth in SEQ ID NOS: 2 ~~or~~ 4.

43. (original) A polypeptide comprising a derivative of the polypeptide of claims 13, 14, or 16.

44. (original) The polypeptide of claim 43 which is covalently modified with a water-soluble polymer.

45. (original) The polypeptide of claim 44 wherein the water-soluble polymer is selected from the group consisting of polyethylene glycol, monomethoxy-polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols, and polyvinyl alcohol.

46-48. (canceled)

49. (original) A fusion polypeptide comprising the polypeptide of claims 13, 14, or 16 fused to a heterologous amino acid sequence.

50. (original) The fusion polypeptide of claim 49 wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

51-57. (canceled)

58. (original) A method of identifying a compound which binds to a polypeptide comprising:

(a) contacting the polypeptide of claims 13, 14, or 16 with a compound;
and

(b) determining the extent of binding of the polypeptide to the compound.

59-66. (canceled)